

# Resource Summary Report

Generated by T1D on Jul 31, 2026

## OSA

RRID:SCR\_002016

Type: Tool

---

### Proper Citation

OSA (RRID:SCR\_002016)

---

### Resource Information

**URL:** <http://wwwchg.duhs.duke.edu/research/osa.html>

**Proper Citation:** OSA (RRID:SCR\_002016)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 19, 2025. Software application that allows the researcher to evaluate evidence for linkage even when heterogeneity is present in a data set. This is not an unusual occurrence when studying diseases of complex origin. Families are ranked by covariate values in order to test evidence for linkage among homogeneous subsets of families. Because families are ranked, a priori covariate cutpoints are not necessary. Covariates may include linkage evidence at other genes, environmental exposures, or biological trait values such as cholesterol, age at onset, and so on.

**Abbreviations:** OSA

**Synonyms:** Ordered Subset Analysis, OSA Program, Ordered Subset Analysis Program

**Resource Type:** software resource, software application

**Defining Citation:** [PMID:18473393](#), [PMID:15185403](#)

**Keywords:** gene, genetic, genomic, c++, unix, solaris, linux

**Funding:** NIMH R01 MH59528

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** OSA

**Resource ID:** SCR\_002016

**Alternate IDs:** nlx\_154504

**Old URLs:** <http://wwwchg.duhs.duke.edu/software/osa.html>

**Record Creation Time:** 20220129T080211+0000

**Record Last Update:** 20260731T042621+0000

---

## Ratings and Alerts

No rating or validation information has been found for OSA.

No alerts have been found for OSA.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Schmidt S, et al. (2004) Ordered subset linkage analysis supports a susceptibility locus for age-related macular degeneration on chromosome 16p12. BMC genetics, 5, 18.